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Bi-segmented regression, factor analysis and AMMI applied to the analysis of adaptability and stability of soybean

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Abstract

The aim of this study was to determine the phenotypic adaptability and stability of the soybeans grown in different environments of Rio Grande do Sul through bissegmented regression analysis, factor analysis and AMMI. The experiment was held in 2013/2014 season in a randomized block design factorial (six environments cultivation × 20 genotypes of soybean), arranged in three replications. The results showed that methods of adaptability and stability have similar responses to the rank of environments. The Tenente Portela - RS, Arroio Grande - RS lowland and coxilha were favorable environments, while Santa Rosa - RS and Campos Borges -RS have been recognized unfavorable for soybean genotypes. Differential responses were obtained for the Sarandi - RS environment, where the factor analysis and regression bissegmented revealed that this is a favorable environment, while the method AMMI indicated negative scores and unfavorable. Genotypes TMG 7161 RR and NA5909 RR were indicated as high productivity and recommended for favorable environments for both methods. To reconcile bissegmented regression, factor analysis and AMMI accurately predicted the best genotypes and environments for soybean.

Keywords: *Glycine max* L., univariate and multivariate analysis, biometrics, breeding.
Abbreviations: AMMI_Additive main effects and multiplicative interaction analysis; NPK_nitrogenio/fósforo e potássio; CFA_subtropica; %_percentual; kg ha^{-1}_kilograms per hectare; m_meters;*yij*_response of genotype *i* at *j* environment; μ_overall average; *gi*_genotypic effect; εj_environmental effect; λk_kth singular value of GE (scalar); γik_ith genotype at vector γk; αjk_jth environment; *pij*_modeler of the GE interaction; ε_{ij}_average experimental error; CV_coefficient of variation.

Introduction

Soybean (*Glycine max* L.) is characterized as an oilseed belonging to the family Fabaceae, playing widespread in the Brazilian agricultural cultivation scenario in the most distinct regions and levels of technologies. It is economically viable to the farmer due to the high productivity and the vast amount of available genotypes. There are many factors responsible for the productivity of soybeans, such as the genotype, the edaphoclimatic characteristics of the environment, the handling practices, and the genotype x environment interaction, which being considered as the most important of them (Rocha et al., 2009).

Facing with the need to indicate which genotypes are more efficient in certain environments, difficulties are attributed to the genotype x environment (G × E) interaction, which is defined as the changes in the response of the genotype to different environments (De Carvalho et al., 2002). These achievements result from the phenotypic inconsistency of genotypes due to environmental differences and fluctuations (Barros et al., 2012). Simple interactions reveals responses with similar meanings of genotypes regarding the environments tested with minor difficulties in the recommendation. However, differential responses culminate in complex interaction with greater influence on the estimation of the parameters of phenotypic adaptability and stability (Cruz et al., 2014). Adaptability is defined as the ability of genotypes to respond positively to better environments, and stability refers to high phenotypic predictability of the genotypes in relation to environmental variations (Cruz et al., 2014). An ideal genotype was determined by Eberhart and Russell (1966) as one that shows high grain yield, phenotypic stability, tolerance to unfavorable environments, and responsiveness to better environments (Cruz et al., 2012). Among the available methods to estimate the parameters of adaptability and stability, bi-segmented regression was developed by Silva and Barreto (1985) and modified by Cruz et al. (1989), based on a linear regression analysis. It looks for the best adjustment equation to estimate the parameters β_0, relating to the average productivity of the genotype, β_1, which shows the linear coefficient for unfavorable environments, $\beta_1+\beta_2$, characterizing favorable environments, and δ^2, which expresses the deviations from the regression and indicates the genotype stability (Cruz et al., 2014). Multivariate techniques can be employed to determine the environmental stratification, where the factor analysis allows revealing which genotypes are widely adapted, and points those are responsive to specific environments (Murakami and Cruz, 2004). It has the premise of genotype grouping through their performance, and reduces the magnitude of the original information in a smaller extract called factors (Mendonça et al., 2007).

The method additive main effects and multiplicative interaction analysis (AMMI) consists of univariate and multivariate statistical techniques, and allows breaking the effects of the GxE interaction (Duarte and Vencovsky, 1999). It enables detailing the effects of the interaction to identify which genotypes contribute positively. In this way, it increases the accuracy of the predicted estimates, and better represent the genotypes and environments through Biplot graphs (Oliveira et al., 2003). Due to the large number of available genotypes and the lack of information regarding the recommendation for the different soybean producing micro-regions, this study aimed to determine the phenotypic adaptability and stability of the soybean grown in different environments of Rio Grande do Sul through the methodologies of bi-segmented regression analysis, factor analysis and AMMI.

Results and Discussion

Characterization of traits

The analysis of variance showed a significant interaction for the six cultivation environments x 20 soybean genotypes ($p<0.05$) for grain yield. The coefficients of variation of the environments were: Santa Rosa - RS (CV: 23.18%), Tenente Portela - RS (CV: 24.54%), Campos Borges - RS (CV: 24.41%), Sarandi - RS (CV: 25.35%), Arroio Grande – RS, lowland (CV: 20.31%) and Arroio Grande – RS, upland (CV: 24.43%). The grain yield shows amplitude of 1995.70 kg ha^{-1} at 4002.30 kg ha^{-1}, with overall average of 3083.32 kg ha^{-1} grains. The results are consistent with the average (3368 kg ha^{-1}) of Rio Grande do Sul for the 2013/2014 harvest (Conab, 2015).

Performance of traits on the grouping of means by Scott-Knott

The grouping of means by Scott-Knott (1974) shows that the genotypes ROOS Camino RR, TMG 7161 RR and FPS Iguaçu RR were superior for grain yield, with 3998.0 kg ha^{-1}; 3860.6 kg ha^{-1} and 3744.3 kg ha^{-1}, respectively. Underperformance was obtained for BRS Tordilha RR and AMS Tibagi RR, with 2263.5 kg ha^{-1} and 2266.5 kg ha^{-1} grains, respectively (Table 2). Grain yield is a quantitative trait controlled by many genes; therefore, it is directly influenced by the G x E interaction, resulting from the joint action of intrinsic characteristics of the genotype, of the edaphoclimatic conditions, photoperiod, rainfall, temperature, relative humidity, and handling practices (Rocha et al., 2009).

Performance of traits on the bi-segmented regression

The bi-segmented regression proposed by Silva and Barreto (1985) and modified by Cruz et al. (1989) has as adaptability parameters the average grain yield of the genotype (β_0) and the linear coefficient for unfavorable environments ($\beta_1<1$) and favorable environments ($\beta_1+\beta_2>1$). On the other hand, stability is determined by the deviation from regression (δ^2) of the genotypes against the environments (Cruz et al., 2014). An ideal genotype must have high grain yield, yield stability, tolerance to unfavorable environment, and responsiveness to better environments (Cruz et al., 2012). The environments were characterized by the environmental index (*Aj*), where Tenente Portela - RS (*Aj*: 919.0), Sarandi - RS (*Aj*: 223.4), Arroio Grande – RS, lowland (*Aj:* 438.5) and Arroio Grande – RS, upland (*Aj*: 181.8) are considered favorable. In contrast, Santa Rosa - RS (*Aj*: -1087.6) and Campos Borges - RS (*Aj*: -675.0) are unfavorable environments. To distinguish which environments are favorable or unfavorable for soybean, it is defined which genotype is specific to a particular environment, with higher grain yield for this genotype under appropriate conditions (Mendonça et al., 2007). All favorable environments obtained a positive environmental index and grain yield higher than the overall average in 22.9; 6.76; 12.4 and 5.57% for Tenente Portela - RS, Sarandi - RS, Arroio Grande – RS, lowland and upland, respectively.

The linear coefficient β_1 indicates the response of genotypes to unfavorable environments ($\beta_1<1$), and shows no significance by t test ($p<0.05$) for all tested genotypes (Table 2). The linear coefficients $\beta_1+\beta_2$ indicate the response of genotypes to favorable environments ($\beta_1+\beta_2>1$), where BMX Potência RR, NA 5909 RR and TMG 7161 RR have adaptability to favorable environments. The genotypes Tenente Portela - RS, Sarandi - RS, Arroio Grande – RS (lowland and upland), increased 6.6% (2982.3 kg ha^{-1}), 12.8% (3511.8 kg ha^{-1}) and 19.0% (3860.6 kg ha^{-1}) of yield under favorable environments, compared to the overall average of the environments.

The stability parameter expressed by the variance of the regression deviations (δ^2) indicates significance for the genotypes and $\delta^2>0$, featuring low phenotypic stability for the tested environments. These genotypes were FPS Iguaçu RR, BMX Potência RR, NA 5909 RR and TMG 7161 RR. The other genotypes were not significantly different and the grain yield averages (β_0) should be considered judiciously. The determination coefficients (R^2) were intermediate, where the behavior of genotypes against the environments was represented by the model proposed by Cruz et al. (1989). The determination coefficients, when less than 0.70, resulted from the increase of the oscillations regarding the cultivation environment (Cruz et al., 2014).

Performance of traits on the factor analysis

Factor analysis is grounded on multivariate tools that allows environmental stratification, and reveals which genotype is widely adapted and responsive to a specific environment, following the assumption that the genotypes are grouped for responding similarly. Results are obtained by the rotation of factors arising from the matrix of factor loadings (Murakami and Cruz, 2004). The analysis was performed for grain yield of 20 genotypes grown in six environments (Table 3). Estimates of the eigenvalues were determined using as a criterion, explaining more than 80% of the total existing variation (Cruz et al., 2014). Thus, it obtained estimates of 83.5% with the use of three final factors. After the rotation of the factor loading, it was used as a criterion for the grouping of environments and magnitude of loadings. When it was above 0.70, it reveals that environments are correlated and allow being grouped; loadings between 0.50 and 0.70 do not allow defining as groups; and loadings of less than 0.50 do not make it possible to cluster environments (Johnson and Wichern, 1992). Factor I had factor loading higher than 0.70 only for Tenente Portela - RS and no grouping was possible, with positive environmental index (*EI*: 918.9), characterized as favorable. Factor II showed higher loads for Sarandi - RS and Arroio Grande - RS (upland), with positive environmental indices (*EI*: 223.4) and (*EI*: 181.8), these being favorable, respectively. Factor III revealed higher loads to Santa Rosa - RS and Campos Borges – RS, with negative environmental indices (*EI*: -1087.6) and (*EI*: -675.0), being unfavorable, respectively.

Table 1. Characterization of cultivation environments according to geographic coordinates, altitude and soil type.

CultivationEnvironments	Geographic Coordinates		Altitude	*Soil Type
	Latitude	Longitude		
Santa Rosa-RS	27º52’S	54º28’O	268 m	Red latosol distroferric
Tenente Portela-RS	27º22’S	53º45’O	420 m	Typical latosol red ferric
Campos Borges-RS	28º55’S	53º01’O	513 m	Red dark latosol
Sarandi-RS	27º55’S	52º56’O	408 m	Typical red latosol distroferric
Arroio Grande - RS (várzea)	32º12’S	53º05’O	22 m	Red-yellow podzolic eutrophic
Arroio Grande - RS (coxilha)				

*The soil classification according Embrapa (2006).

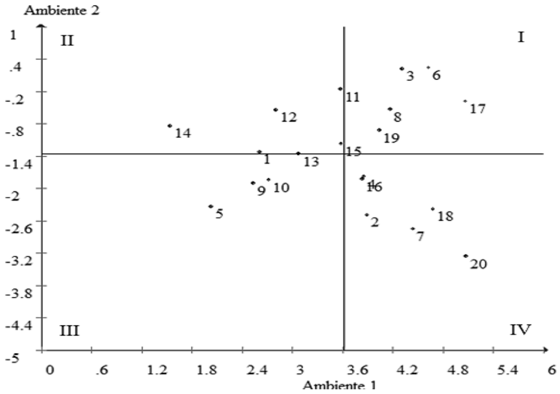

Fig 1. Scores plot considering the factors E (1: Tenente Portela - RS) and II (2: Sarandi - RS and Arroio Grande - RS coxilha) on the results obtained in the analysis of factors to grain yield, referring to 20 genotypes evaluated soy in six cultivation environments in the season 2013/2014 * genotypes:*G1*: BRS Tordilha RR; *G2*: FPS Paranapanema RR; *G3*: Fepagro 37 RR; *G4*: FPS Solimões RR; *G5*: Fepagro 36 RR; *G6*: FPS Netuno RR;*G7*: FPS Iguaçu RR; *G8*: FPS Urano RR; *G9*: FPS Júpiter RR; *G10*: AMS Tibagi RR; *G11*: Don Mario 7.0i RR; *G12*: A6411 RR; *G13*: Don Mario 5.8i RR; *G14*: BMX Potência RR; *G15*: Don Mario 5.9i RR; *G16*: Roos Camino RR; *G17*: BMX Ativa RR; *G18*: NA 5909 RR; *G19*: BMX Turbo RR; *G20*: TMG 7161 RR.

Therefore, the factor analysis shows effectiveness in environmental stratification for the soybean grain yield (Mendonça et al., 2007). Stratification of environments is effective when the experimental factors indicate significant interaction between genotypes x environments, when compared to the interaction genotype x crop years (Oliveira et al., 2005).

The scores were expressed graphically considering the factors I and II regarding the results obtained for grain yield (Fig 1), quadrant I consists of genotypes Fepagro 37 RR, FPS Netuno RR, FPS Urano RR, BMX Ativa RR and BMX Turbo RR, which are characterized as stable and of wide adaptability, and recommended to both factors, being: Sarandi - RS, Arroio Grande - RS (upland) and Tenente Portela - RS. Quadrant II is responsible for grouping the genotypes BRS Tordilha RR, Don Mario 7.0i RR, A6411 RR, Don Mario 5.8i RR, BMX Potência RR, Don Mario 5.9i RR, with adaptability to specific environments representing factor II (Sarandi - RS and Arroio Grande – RS, upland). Quadrant III represents Fepagro 36 RR, FPS Jupiter RR and AMS Tibagi RR, which revealed poor performance and are not recommended for the tested environments. Quadrant IV comprised of FPS Paranapanema RR, FPS Solimões RR, FPS Iguaçu RR, Roos Camino RR, NA 5909 RR and TMG 7161 RR, and featured adaptability to specific environments corresponding to factor I (Tenente Portela - RS). The commonalities for all environments were above 0.75, indicating that the factor analysis estimates are appropriate. Magnitudes above 0.64 are satisfactory and indicate correlation greater than 0.80 between the standard character and the common part (Cruz et al., 2014).

Performance of traits on the AMMI method

The AMMI method is a model of additive main effects and multiplicative interaction, based on the set of univariate and multivariate statistical techniques, adjusting the G x E interaction (Duarte and Vencovsky, 1999). It allows evidencing genotypes with high grain yield, widely adapted, and selecting more supportive environments for the culture. It also enables the decomposition of the effects of the sum of squares of the G x E interaction in the standard fraction, which identifies environments, genotypes, and noise related to experimental errors (Oliveira et al., 2003). The unfolding of the effects of the sum of squares of the G x E interaction (SQ_{GxE}) by AMMI was significant to the first component (IPCA1) responsible for the standard fraction of the information, and to the waste (noise) at 5% probability. The explicable percentage of the SQ_{GxE} by the IPCA1 component was shown to be high (61.67%). The first significant components of the AMMI method explain the most important portion of the G x E interaction (Pereira et al., 2009). The results obtained are appropriate, compared to studies where the IPCA1 estimated for 18 soybean genotypes cultivated in 12 environments corresponds to 36.57% of the $SQ_{(GxE)}$ (Oliveira et al., 2003). Studies on 20 bean genotypes in 22 cultivation environments also has explained 45.90% $SQ_{(GxE)}$ (Melo et al., 2007).

The genotypes that mostly contributed to the G x E interaction were TMG 7161 RR and NA 5909 RR, with the largest positive magnitudes of the scores for IPCA1 in the axis of the interaction (32.04) and (29.76), respectively (Table 4). The chart of the biplot scores shows that the

Table 2. Estimates of adaptability and stability for grain yield (PG), according to the methodology of Cruz, Torres and Vencovsky (1989) for 20 genotypes of soybean cultivation evaluated in six environments in the season 2013/2014.

Grain Yield (PG)							
Soybean Genotypes	Mean cultivation environments			$\beta_{1(i)}$	$\beta 1+\beta_{2(i)}$	δ^2	R² (%)
	General**	Unfavorable	Favorable				
BRS Tordilha RR	2263.5 s	991.2	2899.6	1.3^{ns}	0.2^{ns}	4.6 $10^{5\ ns}$	90.7
FPS Paranapanema RR	2855.4 o	1503.5	3531.4	1.5^{ns}	0.9^{ns}	2.1 $10^{6\ ns}$	74.0
Fepagro 37 RR	3046.3 k	2346.3	3396.2	0.8^{ns}	1.7^{ns}	2.0 $10^{6\ ns}$	58.7
FPS Solimões RR	3159.8 i	2429.1	3525.1	0.8^{ns}	1.6^{ns}	5.4 $10^{5\ ns}$	83.3
Fepagro 36 RR	2379.5 q	1684.2	2727.1	0.7^{ns}	0.1^{ns}	1.1 $10^{6\ ns}$	57.1
FPS Netuno RR	3169.9 h	1992.7	3758.5	1.3^{ns}	1.3^{ns}	2.2 $10^{6\ ns}$	68.5
FPS Iguaçu RR	3744.3 c	2792.0	4220.5	1.1^{ns}	0.9^{ns}	3.7 10^{6*}	48.6
FPS Urano RR	3258.8 g	2177.1	3799.7	1.2^{ns}	0.8^{ns}	1.1 $10^{6\ ns}$	78.4
FPS Júpiter RR	2353.8 r	1882.8	2589.3	0.5^{ns}	1.2^{ns}	9.2 $10^{5\ ns}$	57.5
AMS Tibagi RR	2266.7 s	1028.0	2886.0	1.3^{ns}	0.1^{ns}	5.7 $10^{5\ ns}$	88.5
Don Mario 7.0i RR	2733.0 p	1843.3	3177.9	0.9^{ns}	1.5^{ns}	1.8 $10^{6\ ns}$	62.9
A6411RR	2997.1 l	2415.9	3287.7	0.6^{ns}	0.1^{ns}	1.3 $10^{6\ ns}$	43.8
Don Mario 5.8i RR	3108.1 j	2432.8	3445.8	0.7^{ns}	0.5^{ns}	7.5 $10^{4\ ns}$	95.0
BMX Potência RR	2982.3 m	2588.1	3179.4	0.4^{ns}	1.7*	2.4 10^{6*}	37.5
Don Mario 5.9i RR	3294.6 f	2752.9	3565.4	0.6^{ns}	1.1^{ns}	1.2 $10^{5\ ns}$	92.6
Roos Camino RR	3998.0 a	3361.5	4316.3	0.7^{ns}	1.2^{ns}	1.3 $10^{6\ ns}$	58.6
BMX Ativa RR	3710.9 d	2700.0	4216.4	1.2^{ns}	1.1^{ns}	1.4 $10^{6\ ns}$	74.1
NA 5909 RR	3511.8 e	2613.3	3961.0	0.9^{ns}	3.2*	4.5 10^{6*}	56.7
BMX Turbo RR	2971.9 n	2118.1	3398.8	1.0^{ns}	1.0^{ns}	6.2 $10^{5\ ns}$	83.2
TMG 7161 RR	3860.6 b	2386.8	4597.6	1.5^{ns}	3.1*	4.1 10^{6*}	69.5

Cultivation Environments	Grain yield (PG) (kg ha^{-1})	Environmental Index *(Aj)*	Characterizationof Environments
Santa Rosa-RS	1995.7	-1087.6	Unfavorable
Tenente Portela-RS	4002.3	919.0	Favorable
Campos Borges-RS	2408.3	-675.0	Unfavorable
Sarandi-RS	3306.7	223.4	Favorable
Arroio Grande-RS várzea	3521.8	438.5	Favorable
Arroio Grande-RS coxilha	3265.1	181.8	Favorable

^{ns}no significant at 5% probability of error; * Significant at 5% error probability; β1 (i) linear regression coefficient associated with the unfavorable environment; β1 + β2 (i) linear regression coefficient associated with enabling environments; δ² variance of the regression deviations; R² coefficient of determination; Aj environmental index.
** Means followed the same letter in the column belong to the same group based on the Scott-Knott test (1974) 5% error probability.

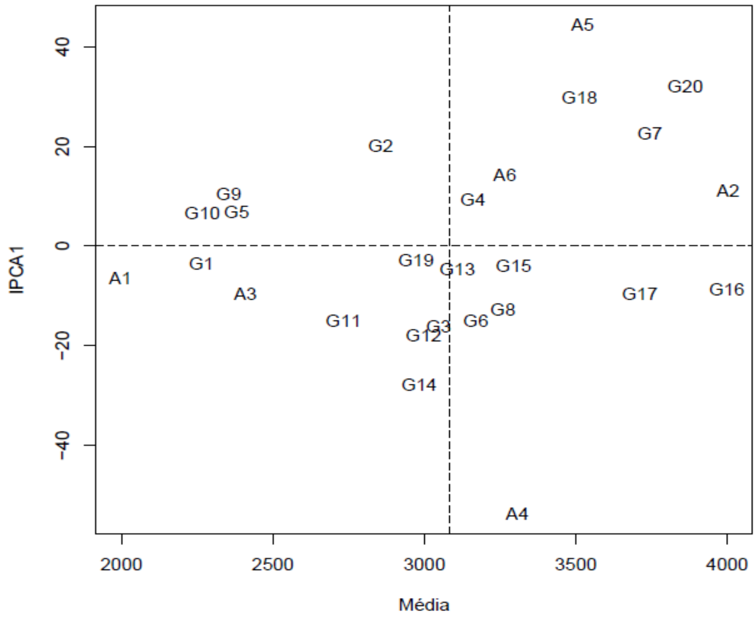

Fig 2. Biplot analysis AMMI for grain yield (kg ha-1) for 20 genotypes of soybean (G) evaluated in six cultivation environments (A) in the season 2013/2014 * genotypes: *G1*: BRS Tordilha RR; *G2*: FPS Paranapanema RR; *G3*: Fepagro 37 RR; *G4*: FPS Solimões RR; *G5*: Fepagro 36 RR; *G6*: FPS Netuno RR; *G7*: FPS Iguaçu RR; *G8*: FPS Urano RR; *G9*: FPS Júpiter RR; *G10*: AMS Tibagi RR; *G11*: Don Mario 7.0i RR; *G12*: A6411 RR; *G13*: Don Mario 5.8i RR; *G14*: BMX Potência RR; *G15*: Don Mario 5.9i RR; *G16*: Roos Camino RR; *G17*: BMX Ativa RR; *G18*: NA 5909 RR; *G19*: BMX Turbo RR; *G20*: TMG 7161 RR.**ambientes: *A1*: Santa Rosa - RS; *A2*: Tenente Portela - RS; *A3*: Campos Borges - RS; *A4*: Sarandi - RS; *A5*: Arroio Grande – RS várzea; *A6*: Arroio Grande – RS coxilha.

Table 3. Factor analysis summary for grain yield (PG) for 20 genotypes of soybean cultivation evaluated in six environments in the season 2013/2014.

Grain yield (PG)								
Estimates of the eigenvalues			Cultivation Environments	Factor loadings after rotation				
Raiz	(%) Raiz	(%) Acumulada		Fator I	Fator II	Fator III	Com[1]	IA[2]
2,84	47,31	47,31	Santa Rosa- RS	0,14	-0,12	0,91	0,86	-1087,63
1,65	27,50	74,81	Tenente Portela- RS	0,90	-0,10	0,29	0,91	918,99
0,53	8,78	83,59	Campos Borges- RS	0,49	0,11	0,73	0,78	-675,04
0,46	7,65	91,24	Sarandi- RS	0,15	0,77	0,49	0,85	223,41
0,33	5,57	96,81	Arroio Grande- RS várzea	0,66	-0,65	0,11	0,87	438,46
0,19	3,19	100,00	Arroio Grande- RS coxilha	0,29	-0,74	0,34	0,75	181,82

[1](*Com*)comunalidades;[2](*IA*) environmental index.

Table 4. Estimated adaptability parameters and phenotypic stability obtained by AMMI for 20 genotypes of soybean cultivation evaluated in six environments in the season 2013/2014.

Cultivation Environments		Grain yield (kg ha^{-1})	AMMI IPCAI
Santa Rosa – RS	E1	1995.71	-6.47
Tenente Portela – RS	E2	4002.31	11.17
Campos Borges – RS	E3	2408.28	-9.60
Sarandi – RS	E4	3306.73	-53.70
Arroio Grande – RS várzea	E5	3521.78	44.28
Arroio Grande – RS coxilha	E6	3265.14	14.33
Genotypes			
BRS Tordilha RR	G1	2263.5 s	-3.61
FPS Paranapanema RR	G2	2855.4 o	20.19
Fepagro 37 RR	G3	3046.3 k	-16.02
FPS Solimões RR	G4	3159.8 i	9.41
Fepagro 36 RR	G5	2379.5 q	6.91
FPS Netuno RR	G6	3169.9 h	-14.96
FPS Iguaçu RR	G7	3744.3 c	22.54
FPS Urano RR	G8	3258.8 g	-12.75
FPS Júpiter RR	G9	2353.8 r	10.37
AMS Tibagi RR	G10	2266.7 s	6.67
Don Mario 7.0i RR	G11	2733.0 p	-15.02
A6411RR	G12	2997.1 l	-18.00
Don Mario 5.8i RR	G13	3108.1 j	-4.69
BMX Potência RR	G14	2982.3 m	-27.86
Don Mario 5.9i RR	G15	3294.6 f	-4.03
Roos Camino RR	G16	3998.0 a	-8.61
BMX Ativa RR	G17	3710.9 d	-9.49
NA 5909 RR	G18	3511.8 e	29.76
BMX Turbo RR	G19	2971.9 n	-2.83
TMG 7161 RR	G20	3860.6 b	32.04

genotypes with specific adaptability and higher grain yield than the overall average of the experiment were TMG 7161 RR, NA 5909 RR, FPS Iguaçu RR and FPS Solimões RR (Fig 2). The stable genotypes in different environments revealed low and positive scores, with lower contribution to the interaction, being stable and greater than the overall average, such as Don Mario 5.9i RR and Don Mario 5.8i RR. On the other hand, those stable and lower than the average were BRS Tordilha RR, Fepagro 36 RR, AMS Tibagi RR and BMX Turbo RR. General adaptability was expressed by Fepagro RR 36 and AMS Tibagi RR, being close for Santa Rosa - RS and Campos Borges - RS. The Arroio Grande - RS (lowland) environment contributed positively to the interaction with high and positive scores (44.28). In contrast, negative scores are obtained in Santa Rosa - RS (-6.47), Campos Borges - RS (-9.60) and Sarandi - RS (-53.70), as unfavorable. Tenente Portela - RS (11.17) and Arroio Grande - RS (upland) (14.33) are presented as stable in environments, with low and positive scores compared to the tested environments.

By linking the methods used in the analysis of soybean genotypes, similar responses were observed in Santa Rosa - RS and Campos Borges – RS as unfavorable, and Tenente Portela – RS and Arroio Grande - RS (lowland and upland), as favorable. The methods based on regression analysis and AMMI, when used together, allow greater efficiency in the estimation of the phenotypic stability and adaptability of soybean (Junior and Silva, 2005). Distinctions regarding the methods are presented for the Sarandi - RS environment, where bi-segmented regression analysis and factor analysis characterize it as favorable, although the AMMI method has negative IPCA1 scores and indicates an unfavorable environment. Studies carried out in 34 environments and ten potato genotypes show that the estimates obtained by bi-segmented regression are more efficient than those of the AMMI method (Souza et al., 2007). With regard to the performance of the genotypes against the methods used, similar responses were obtained for TMG 7161 RR and NA 5909 RR, recommended for favorable environments. The bi-segmented regression analysis presented absence of significance, and similar responses to factor analysis and AMMI, by which FPS Solimões RR and FPS Iguaçu RR, were found to be favorable for environments. Discrepancy by factor analysis and between the recommendations found

Fepagro 36 RR and AMS Tibagi RR as low performance. In contrast, , they were indicated as of widely adaptible by the AMMI method. For the genotypes Don Mario 5.8i RR and Don Mario 5.9i RR, the factor analysis shows adaptability to favorable environments; though by AMMI method, these genotypes were indicated as stable. The results obtained by bi-segmented regression analysis, factor analysis and AMMI method to distinguish adapted or stable soybean genotypes for the tested environments, shows that for more accurate recommendations and reducion of errors assigned to the genotype x environment interaction, the breeder must jointly use these biometric techniques to indicate the genotypes with greater accuracy to the best environments.

Materials and Methods

Plant materials

The experiments were performed in the 2013/2014 harvest in Santa Rosa-RS, Tenente Portela-RS, Campos Borges-RS, Sarandi-RS and Arroio Grande-RS (lowland and upland). The climate is characterized by Köppen as subtropical *Cfa* and other characteristics of the farming environments are shown in Table 1.

Experimental design and experimental procedure

The experimental design was randomized blocks, arranged in a factorial with six cultivation environments × 20 genotypes of soybean, in three replications. Genotypes were: BRS Tordilha RR, FPS Paranapanema RR, Fepagro 37 RR, FPS Solimões RR, Fepagro 36 RR, FPS Netuno RR, FPS Iguaçu RR, FPS Urano RR, FPS Júpiter RR, AMS Tibagi RR, Don Mario 7.0i RR, A 6411 RR, Don Mario 5.8i RR, BMX Potência RR, Don Mario 5.9i RR, ROOS Camino RR, BMX Ativa RR, NA 5909 RR, BMX Turbo RR and TMG 7161 RR.

The direct seeding system was used in all environments, being implemented in the second half of November 2013. The basic fertilization was 250 kg ha^{-1} NPK in the formulation 02-20-20, and the population density established with 300,000 p ha^{-1} in all environments. The experimental unit had four sowing lines, which were five meters long, spaced 0.50m. The two central lines were considered as useful area for evaluations. The control of weeds, insect pests and diseases was conducted in a preventive manner, minimizing biotic effects on the outcome of the experiment. Manual harvesting was conducted in the first half of April 2014, measuring the number of plants harvested per each experimental unit.

Traits measured

The grain yield was obtained from the total mass of grains, with moisture correction to 13%, and it was determined the ratio between the mass of grains and the number of harvested plants. The mass of grains per plant was adjusted to the population density used in the experiment (Carvalho et al., 2015), with results in kg ha^{-1}.

Statistical analysis

The data obtained were subjected to individual analysis of variance in order to verify the assumptions. The normality test of Shapiro-Wilk (1965) and homogeneity of variances by Bartlett test (Steel et al., 1997) were also used. A joint analysis of the cultivation environments x soybean genotypes was performed to verify the interaction of factors at 5% probability. To distinguish the performance of genotypes, it was proceeded the grouping of means by Scott and Knott (1974). Tthe bi-segmented regression analysis was determined according to Cruz et al. (1989), where the adaptability parameters β_0, β_1, and $\beta_1+\beta_2$, and for stability, δ^2 and R², were estimated through the model $yij = \beta_{0i} + \beta_{1i} I_j + \beta_{2i}\ T\left(I_j\right) + \delta_{ij} + \varepsilon_{ij}$, where: y_{ij}: response of genotype i at j environment; β_{0i}: overall average of the genotype; β_{1i}: linear regression coefficient; I_j: environmental index; β_{2i}: regression coefficient associated with $T(I_j)$; δ_{ij}: deviation fromregression; ε_{ij}: average experimental error (Cruz et al., 2012).

The analysis of adaptability and environmental stratification was performed by Murakami & Cruz (2004). The Additive main effects and multiplicative interaction analysis (AMMI) method was based on the model $yij = \mu + g_i + \varepsilon_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$, where: yij: response of genotype i at j environment; μ: overall average; gi: genotypic effect; εj: environmental effect; λk: kth singular value of GE (scalar); γik: ith genotype at vector γk; αjk: *jth* environment; pij: modeler of the GE interaction; ε_{ij}: average experimental error (Duarte and Vencovsky, 1999). Statistical analyses were performed using the software Genes (Cruz et al., 2013) and R program (version 3.1.3) (R Core Team, 2015).

Conclusion

The methods of adaptability and stability have similar responses to the classification of the environments Tenente Portela - RS, Arroio Grande - RS (lowland and upland) as favorable, *versus* Santa Rosa - RS and Campos Borges - RS as unfavorable to soybean genotypes. Differential responses were obtained for the Sarandi - RS environment, where the factor analysis and the bi-segmented regression revealed that this is a favorable environment, while the AMMI method indicates negative and unfavorable scores. Genotypes TMG 7161 RR and NA 5909 RR were distinguished as of high productivity and recommended for favorable environments by both methods. The combination of bi-segmented regression, the factor analysis and the AMMI, enables breeders to more accurately predict what are the best genotypes and environments for the soybean.

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